

GenCore version 4.5  
 Copyright (c) 1993 - 2000 Compugen Ltd.  
 OM nucleic - nucleic search, using sw model  
 Run on: May 24, 2002, 19:15:39 ; search time 1997.16 seconds  
 (without alignments)  
 3981.696 Million cell updates/sec

Title: W36511  
 Perfect score: 380  
 Sequence: 1 GCAAGCGCAGCAGCTCC... . . . . . ACTTATTATTACCAATGAC 380  
 - Scoring table: IDENTITY\_NUC  
 Gapop 11.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
 Total number of hits satisfying chosen parameters: 3595312  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

listing first 45 summaries

Database : GenEmbI:  
 1: qb\_ba: \*  
 2: qb\_htg: \*  
 3: qb\_in: \*  
 4: qb\_on: \*  
 5: qb\_ov: \*  
 6: qb\_Pat: \*  
 7: qb\_Ph: \*  
 8: qb\_DL: \*  
 9: qb\_Pt: \*  
 10: qb\_RO: \*  
 11: qb\_STS: \*  
 12: qb\_SY: \*  
 13: qb\_UN: \*  
 14: qb\_VI: \*  
 15: em\_ba: \*  
 16: em\_fun: \*  
 17: em\_hum: \*  
 18: em\_in: \*  
 19: em\_mu: \*  
 20: em\_on: \*  
 21: em\_or: \*  
 22: em\_ov: \*  
 23: em\_Pat: \*  
 24: em\_ph: \*  
 25: em\_Pl: \*  
 26: em\_RO: \*  
 27: em\_STS: \*  
 28: em\_un: \*  
 29: em\_vl: \*  
 30: em\_htg\_hum: \*  
 31: em\_htg\_inv: \*  
 32: em\_htg\_other: \*  
 33: em\_htg\_inv: \*

ALIGMENTS

RESULT 1  
 MM14334 MMY14334 2347 bp mRNA linear ROD 11-MAR-1999  
 LOCUS MUS\_musculus mRNA for arachidonate 12-lipoxygenase, 12R-type.  
 DEFINITION MUS\_musculus mRNA for arachidonate 12-lipoxygenase, 12R-type.  
 ACCESSION Y14334  
 VERSION Y14334.1  
 KEYWORDS G1;3043452  
 SOURCE 12(R)-lipoxygenase; Alox12B gene; arachidonate 12-lipoxygenase.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. (bases 1 to 2347)  
 1 (bases 1 to 2347)  
 Krieg, P.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query	Match Length	DB	ID
SUMMARIES					
REMARK					
REFERENCE					
AUTHORS					
TITLE					
CDNA cloning of a 8-lipoxygenase and a novel epidermis-type lipoxygenase from phorbol ester-treated mouse skin					
Biochim. Biophys. Acta 1391 (1), 7-12 (1998)					
JOURNAL					

MEDLINE	98186642	REFERENCE	(bases 1 to 2347)
3		AUTHORS	Krieg, P., Schubert, M., Kinzig, A., Marks, F. and Fuerstenberger, G.
TITLE	Murine 12(R)-lipoxygenase: functional expression, genomic structure and chromosomal localization	AUTHORS	
JOURNAL	unpublished	REFERENCE	
FEATURES	Location/Qualifiers	1.	2347
source		/organism="Mus musculus"	
		/strain="NMR1"	
		/db_xref="taxon:10090"	
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		/tissue_type="skin epidermis"	
		/clone_id="TPA-treated epidermis CDNA in lambda ZAP1"	
gene		/gene="Alox12b"	
		176..2331	
CDS		/note="12R-type"	
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		/note="SPTRIMBL:070582"	
		/translation="MATAVKVVAQGDFESGTLDSISLTIVGTOGESHKQRQLNHFGRD	
		FATGAVDDYVYVQOCQDGLGELIIRHKHPSFLAKDPWCVNYVQICAPCRVHFPAI	
		OMWDGTYETLALREATGKTTADDPFLILHKEHPSFLAKDPWCVNYVQICAPCRVHFPAI	
		SYHPPRRCRNPNEWDGVPYIGPILINIKATRFLNSLRLSEVKTAAFFYRUGPMA	
		LAFKJGLGLDKRSKWRKDKNIFKPNVSEKVAHTEDEFFGQYKINGNPL	
		IRRCNQIPDKPFPVTDENMMPAIAQSOPTPDCPFLPLNPNSEWDMLAKWVWRAEFYS	
		HHCAPMCLLPGDQGMMMPAIAQSOPTPDCPFLPLNPNSEWDMLAKWVWRAEFYS	
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		TCVWVNTCSARHAWNSQOLEYTSWMPNPFSMNPQMTGKLTQMDTIPDVK	
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BASE COUNT	517	a	688
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Best Local Similarity	98.5%	DB	10;
Matches	199;	Length	2347;
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Mismatches	2;		
Indels	1;		
Gaps	1;		
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Gaps	1;		
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Conservative	0;		
Mismatches	3;		
Indels	1;		
Gaps	1;		
BASE COUNT	3	UTR	
ORIGIN			
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Conservative	0;		
Mismatches	3;		
Indels	1;		
Gaps	1;		
BASE COUNT	3	UTR	
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Best Local Similarity	98.0%	DB	10;
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Conservative	0;		
Mismatches	3;		
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Gaps	1;		
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Gaps	1;		
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Indels	1;		
Gaps	1;		
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Indels	1;		
Gaps	1;		
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Conservative	0;		
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Gaps	1;		
BASE COUNT	3	UTR	
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Gaps	1;		
BASE COUNT	3	UTR	
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Gaps	1;		
BASE COUNT	3	UTR	
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Gaps	1;		
BASE COUNT	3	UTR	
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Mismatches	3;		
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Gaps	1;		
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Gaps	1;		
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Gaps	1;		
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Mismatches	3;		
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Gaps	1;		
BASE COUNT	3	UTR	
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Gaps	1;		
BASE COUNT	3	UTR	
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Mismatches	3;		
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Gaps	1;		
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Gaps	1;		
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Mismatches	3;		
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Gaps	1;		
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Mismatches	3;		
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Gaps	1;		
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Best Local Similarity	98.0%	DB	10;
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Gaps	1;		
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Mismatches	3;		
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Gaps	1;		
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Gaps	1;		
BASE COUNT	3	UTR	
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Best Local Similarity	98.0%	DB	10;
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Mismatches	3;		
Indels	1;		
Gaps	1;		
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Conservative	0;		
Mismatches	3;		
Indels	1;		
Gaps	1;</		

RESULT 3  
 AL645902 LOCUS AL645902  
 DEFINITION Mus musculus chromosome 11 clone RP23-1912, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, in ordered pieces.  
 ACCESSION AL645902  
 VERSION AL645902.5 GI:17903578  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 REFERENCE  
 AUTHORS Lovell,J.  
 TITLE Direct Submission  
 JOURNAL  
 COMMENT Submitted (17-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquer@sanger.ac.uk. On Dec 18, 2001 this sequence version replaced gi:17736621.  
 Center: Wellcome Trust Sanger Institute  
 Web site: http://www.sanger.ac.uk  
 Contact: humquer@sanger.ac.uk  
 ----- Project Information  
 Center project name: bm192  
 ----- Summary Statistics  
 Assembly program: xGAP4; version 4.5  
 Sequencing vector: plasmid; 100% of reads  
 Chemistry: dye-terminator Big Dye; 100% of reads  
 Consensus quality: 183739 bases at least Q40  
 Consensus quality: 183756 bases at least Q30  
 Insert size: 183759; sum-of-contigs  
 Insert size: 190781; 2.6% error; agarose-fp  
 Quality coverage: 17.34x in Q20 bases; sum-of-contigs Quality coverage: 16.70x in Q20 bases; agarose-fp  
 \* NOTE: This is a 'working draft' sequence.  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
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 /note="assembly\_fragment:02187  
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 BASE COUNT 45953 a 44588 c 44502 g 48716 t  
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 1. 183759  
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 /vector\_side:right"  
 BASE COUNT 45953 a 44588 c 44502 g 48716 t  
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 Best local Similarity 99.4%; Pred. No. 1.1e-31; Mismatches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 175 TTTCCCTGGGCTTAGGGCTTGGACAGGGATTCGGGCTGCTCGAGCTCACC  
 Db 182008 TGTCCCTGGGCCATGAGGGCTTGGACAGGGATTCGGGCTGCTCGAGCTCACC 182067  
 QY 235 ACAAAAGCTCTGCACTCCAAACGACTTGGAGGGGGGTCAGGACCTGCTGGGT  
 Db 182008 ACAAAAGCTCTGCACTCCAAACGACTTGGAGGGGGTCAGGACCTGCTGGGT 182127  
 QY 295 ATTTTCCGATGAGAGCTGGCTGTTGGTACCGATGAGGGT 342  
 Db 182128 ATTTTCCGATGAGAGCTGGCTGCTGGTACCGATGAGGGT 182175

RESULT 4  
 AL65527 LOCUS AL645527  
 DEFINITION Mus musculus chromosome 11 clone RP23-2616, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, in unordered pieces.  
 ACCESSION AL645527  
 VERSION AL645527.12 GI:1825051  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 REFERENCE  
 AUTHORS 1 (sites)  
 TITLE Ashwell,R.  
 JOURNAL  
 COMMENT Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquer@sanger.ac.uk. On Jan 19, 2002 this sequence version replaced gi:18152591.  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquer@sanger.ac.uk  
 ----- Project Information  
 Center project name: bm616  
 ----- Summary Statistics  
 Assembly program: xGAP4; version 4.5  
 Sequencing vector: plasmid; 108752; 100% of reads  
 Chemistry: dye-terminator Big Dye; 100% of reads  
 Consensus quality: 25745 bases at least Q40  
 Consensus quality: 25813 bases at least Q30  
 Consensus quality: 25869 bases at least Q20  
 Insert size: 259831; sum-of-contigs  
 Insert size: 221534; 8.6% error; agarose-fp  
 Quality coverage: 8.13x in Q20 bases; sum-of-contigs Quality coverage: 9.54x in Q20 bases; agarose-fp  
 \* NOTE: This is a 'working draft' sequence.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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 misc\_feature  
 1. 261031  
 /note="assembly\_fragment:03026  
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 1. 18204  
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 1. 3926  
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 1. 52548  
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 1. 52649  
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 /vector\_side:right"  
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 /clone\_end:T7  
 /vector\_side:right"  
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 1. 141677  
 /note="assembly\_fragment:02429

misc_feature	fragment_chain:1	/gene="ALOX12B" /codon_start=1 /product="12-lipoxygenase" /protein_id="AA79680.1" /db_xref="GI:398783" /translation="MANYKIVVATGTDLSSGTRDSISLTIVGTOCESHKKLLNHFGRD FATGAVQYTVQCPDQIGELITRHKERAFFPDPWNYVOLCAPNQRTYRPPAY OMNDGYETLALREATGKTTADSDPVLHEKRETRAKQDFYHWRVFLPGLPSVHIF SYRPVRRHNPWPKWYIPGFPILINRFLNRYSFILKSVYEAHQAEDEFGYOLVNGNPL LAFKVRGLLICKHSWKLKDTRKFGKKSVSEVAAHQAEDEFGYOLVNGNPL TRCTRIPDKFVTDKNAVPAFGEGLCQDLEKGNLYLADYRMEGIPVNGL HRGAPICLHLGPPGEGKAMPITAIQSLQPPCPFIRPSDWDWLAKTQWRYAFY HEIAHLETHIIAEFLCALLRNLPMPHPIYKLLIPHTRTWVOLNSIGAVLNEGG L8AKGMSIGVVEFAGAVRALSLETDLSLIPDNEVERGQDLYYRPLDSLAWNA LEKVYTEITTYTYPDSAVVEGDPLEOSWQELKFCULGRGSSGFPCRLKVPYJL VTVIVIVCSAKIARAVNGOMEETAWHNPFPASMRNPNIPIQKGLTLETFDTPLPVKT TCITLIVWVILSREPDDRPPLQHEDPDIHVEEAPRSIEAFQRQINQSHDQRNKC LPIYYVYDPLVLENISI"
misc_feature	fragment_chain:2	/note="assembly_fragment:01853 fragment_chain:2" /note="assembly_fragment:00080 fragment_chain:2" /note="assembly_fragment:01558 /note="assembly_fragment:01068 /note="assembly_fragment:261031 /note="assembly_fragment:01558 /note="assembly_fragment:01558
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ORIGIN		
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Best Local Similarity	99.4%	Pred. No. 1.e-31; Mismatches 0; Indels 1; Gaps 0;
Matches	167;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	175	TTTCCCCTGGCCCTAGAGGCTCGACAGGTGATGGTCTGGGGCTGTCCTGGCTACCT 234
Db	82649	TGTCCTGGCCCTAGAGGCTCGACAGGTGATGGTCTGGGGCTGTCCTGGCTACCT 82708
QY	235	ACAAAGCCTCTGATTCACAGACTTGTGAGGCGGGGTCAGACCTGCCCTGGT 294
Db	82709	ACAAAGCCTCTGATTCACAGACTTGTGAGGCGGGGTCAGACCTGCCCTGGT 82768
QY	295	ATTATTCGGTGTGACAGCAGCTGGCTACCGATGGAGGT 342
Db	82769	ATTATTCGGTGTGACAGCAGCTGGCTACCGATGGAGGT 82816
RESULT	5	
AF059250	AF059250	2278 bp mRNA, linear PR 27-NOV-1998
LOCUS		
DEFINITION	Homo sapiens lipoxygenase (ALOX12B) mRNA, complete cds.	
ACCESSION	AF059250	
VERSION	AF059250.1	GI:3928782
KEYWORDS		
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ORGANISM	Human.	
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 2278)	
AUTHORS	Sun, D., Mcbonell, M., Chen, X.S., Iakkis, M.M., Li, H., Isaacs, S.N., Elsea, S.H., Patel, P.R. and Funk, C.D.	
TITLE	Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning, expression, and gene chromosomal assignment	
JOURNAL	J. Biol. Chem. 273 (50), 33540-33547 (1998)	
MEDLINE	99057919	
REFERENCE	2 (bases 1 to 2278)	
AUTHORS	Sun, D. and Funk, C.D.	
TITLE	Direct submission	
JOURNAL	Submitted (13-APR-1998) Pharmacology, University of Pennsylvania, 422 Curie Blvd., Philadelphia, PA 19104, USA	
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Db	1404	TGTCCTGGCCCTAGAGGCTCGACAGGTGATGGTCTGGGGCTGTCCTGGT 1463
QY	235	ACAAAGCCTCTGATTCACAGACTTGTGAGGCGGGGTCAGACCTGCCCTGGT 294
Db	1464	ATGAGCCCTACTCCCAAAGTACTTGTGAGGCGGGGTCAGACCTGCCCTGGT 1523
QY	295	ATTATTCGGTGTGACAGCAGCTGGCTACCGATGGAGGTACGTACTAGAG 354
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QY	355	ATCATCACTATTATC 373
Db	1583	ATCATCACTATTATC 1601
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LOCUS	AR106047	
DEFINITION	Sequence 1 from patent US 6103496.	
ACCESSION	AR106047	
VERSION	AR106047.1	GI:12820112
VERSION		
KEYWORDS		
SOURCE		
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 2469)	
AUTHORS	Brash, A.R., Boenigk, W.E. and Kim, R.B.	
TITLE	Isolated and purified 12R-lipoxygenase protein and nucleic acids	
JOURNAL	Patent: US 6103496-A 1 15-AG-2000; Location/Qualifiers	
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QY	235	ACAAAGCCTCTGCATTCACACGACTTGGGACCGCGGGTCAAGGACTGGCTGGGT	294	Db	1626	TGTCCCTGGGGTGGAGGCTTGGCTGGGTAGGGCTCTGGGGCTACCT	1685
Db	1686	ATGACAGCCCTCTACCTCCCAATGACTTGGGACCGCGGGTCAAGGACTGGCTGGGT	1745	QY	235	ACAAAGCCTCTGCATTCACACGACTTGGGACCGCGGGTCAAGGACTGGCTGGGT	294
QY	295	ATTATTCGGTATGACAGCCGGTGGTGTAGCGAGGGTAGGTGACTAGAG	354	Db	1686	ATGACAGCCCTCTACCTCCCAATGACTTGGGACCGCGGGTCAAGGACTGGCTGGGT	1745
Db	1746	ATTACTACCGCGATGAGACTGGCGGTGGAATGCACTGGAGAGTATGTGAC-GGAG	1804	QY	295	ATTATTCGGTATGACAGCCGGTGGTGTAGCGAGGGTAGGTGACTAGAG	354
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RESULT	7			Db	1805	ATCATCACCTATTATTAC	1823
• AF038461				RESULT	8		
DEFINITION		AF038461	2469 bp mRNA complete cds.	LOCUS	HSA305027		
ACCESSION		Homo sapiens		DEFINITION	Homo sapiens partial ALOX12B gene for arachidonate 12R-lipoxygenase, exons 3 to 14 and partial ALOX15P pseudogene for arachidonate 15-lipoxygenase, exons 11 to 14.		
VERSION		AF038461.1	GI:3220165	ACCESSION	AJ305027		
SOURCE		human.		KEYWORDS	ALOX12B gene; ALOX15P pseudogene; arachidonate 12R-lipoxygenase; arachidonate 15-lipoxygenase.		
ORGANISM		Homo sapiens		SOURCE	Homo sapiens		
REFERENCE	1	(bases 1 to 2469)		ORGANISM	Homo sapiens	13652 bp	DNA linear
AUTHORS	Boeglin,W.E., Kim,R.B. and Brash,A.R.			DEFINITION	Homo sapiens partial ALOX12B gene for arachidonate 12R-lipoxygenase, exons 3 to 14 and partial ALOX15P pseudogene for arachidonate 15-lipoxygenase, exons 11 to 14.		
TITLE	A 12R-lipoxygenase in human skin: mechanistic evidence, molecular cloning, and expression			REFERENCE	AJ305027.1	GI:13374920	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (12), 6744-6749 (1998)			AUTHORS	Krieg,P., Marks,F. and Fuerstenberger,G.		
MEDLINE	98284002			TITLE	A gene cluster encoding human epidemis type lipoxygenases at chromosome 17p13.1: Cloning, physical mapping, and expression		
REFERENCE	2	(bases 1 to 2469)		JOURNAL	Unpublished		
AUTHORS	Boeglin,W.E., Jisaka,M., Kim,R.B. and Brash,A.R.			REFERENCE	2 (bases 1 to 13652)		
TITLE	Direct Submission			AUTHORS	Krieg,P.R.		
JOURNAL	Submitted (14-DEC-1997) Clinical Pharmacology, Vanderbilt University, MBII R4510, 23rd Ave S. at Pierce, Nashville, TN 37232-6602, USA			TITLE	Direct Submission		
FEATURES		Location/Qualifiers		JOURNAL	Submitted (18-AUG-2000) Krieg,P.R., Research Program on Tumor Cell Regeneration, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, Heidelberg, D-69120, GERMANY		
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 ORGANISM: *homo\_sapiens*  
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REFERENCE: 1 (bases 1 to 159582)  
 AUTHORS: Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE: *Homo sapiens*, clone RP11-1D5  
 JOURNAL: *Unpublished*  
 REFERENCE: 2 (bases 1 to 159582)  
 AUTHORS: Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domini, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardiner, S., Grant, B., Haeford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Kafatos, A., Klein, J., Lebochki, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McFarren, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollicino, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
 TITLE: *JOURNAL*  
 JOURNAL: *Submitted (17-Nov-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA*  
 COMMENT: All repeats were identified using RepeatMasker: Smit, A. F. A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIBR  
 Contact: <http://www-seq.wi.mit.edu>  
 Center project name: L1433  
 Center clone name: L D 5  
 ----- Summary Statistics -----  
 Sequencing vector: M13; N77815; 49% of reads  
 Chemistry: Dye-terminator; Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 155110 bases at least Q40  
 Consensus quality: 156900 bases at least Q30  
 Consensus quality: 157688 bases at least Q20  
 Insert size: 119000; agarose-fp  
 Insert size: 158382; sum of contigs  
 Quality coverage: 10.7 in Q20 bases; agarose-fp  
 Quality coverage: 8.1 in Q20 bases.  
 \* NOTE: This is a working draft sequence. It currently  
 \* consists of 13 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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 \* 2921 3020: gap of 100 bp  
 \* 3021 6226: contig of 3204 bp in length  
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 \* 19153 19252: gap of 100 bp  
 \* 19253 73423: contig of 54171 bp in length  
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 DEFINITION Mus musculus Alox12B gene 5' flanking region  
 LINEAR  
 ROD 14-APR-1999

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exons 5 to 11.	830. . 1002
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AUTHORS	830. . 1002
Krieg, P., Marks, F. and Fuerstenberger, G.	830. . 1002
TITLE	830. . 1002
A gene cluster encoding human epidermis-type lipoxygenases at chromosome 17p13.1: Cloning, physical mapping, and expression	830. . 1002
unpublished	830. . 1002
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REFERENCE	830. . 1002
AUTHORS	830. . 1002
Krieg, P.R.	830. . 1002
TITLE	830. . 1002
Submitted (18-AUG-2000) Krieg, P.R., Research Program on Tumor Cell Regulation, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, Heidelberg, D-69120, GERMANY	830. . 1002
JOURNAL	830. . 1002
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length	4293;

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AUTHORS	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 36006)			
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.			
TITLE	Human sapiens chromosome 17, clone CTD-3051C7			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 36006)			
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Brown,A., Camarota,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearbano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,M., Gord,S., Goyette,L., Grand-Pierre,N., Haggas,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatsas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehozic,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T., Menga,V., Murphy,T., Nayor,J., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunhang,P., Pierre,N., Pollara,V., Raymond,C., Rettig,R., Rieback,M., Riley,R., Riese,C., Rogov,P., Roman,J., Rosett,M., Roy,A., Santos,R., Schaefer,S., Schuback,R., Seaman,S., Severi,P., Spender,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wynn,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.			
JOURNAL	Submitted (24-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA			
COMMENT	All repeats were identified using RepeatMasker: Smit, A.F.A., Green, P. (1996-1997), <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a>			
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Center	Whitehead Institute/MIT Center for Genome Research			
Center code	WIBR			
Web site	<a href="http://www-seg.wi.mit.edu">http://www-seg.wi.mit.edu</a>			
Contact	<a href="mailto:sequence_submissions@genome.wi.mit.edu">sequence_submissions@genome.wi.mit.edu</a>			
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Center project name	L23044			
Center clone name	3051_C_7			
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* NOTE: This record contains 46 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely				
* arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and a overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event the record is updated, the accession number will be preserved.				
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17930 18029: gap of 100 bp				
18030 18174: contig of 685 bp in length				
18175 18814: gap of 100 bp				
18815 19492: contig of 678 bp in length				
19493 19592: gap of 100 bp				
19593 20277: contig of 685 bp in length				
20278 20377: gap of 100 bp				
20378 21036: contig of 659 bp in length				
21037 21136: gap of 100 bp				
21137 21817: contig of 681 bp in length				
21818 21917: gap of 100 bp				
21918 22601: contig of 684 bp in length				
22602 22701: gap of 100 bp				
22702 23377: contig of 676 bp in length				
23378 23477: gap of 100 bp				
23478 24172: contig of 681 bp in length				
24173 24272: gap of 100 bp				
24273 24927: contig of 655 bp in length				
24928 25027: gap of 100 bp				
25028 25809: contig of 782 bp in length				
25810 25909: gap of 100 bp				





Maye 14

ARATLNPEGLYDQVISIGROGLIYLMSTGLAHFTYNTFCILDLSRARGVLAIPNHY  
RODGKIKWAESFVSBEIVGYYPSDASVQDSELQWATGEEIFAAFLGEESSGIPSR  
LCTPGENVKFTTAIFNCSAHAAVNSOHFGAWMPNATSSMRQOPPQQTGTTLKI  
YDTPPEVNITCNLNUFLWMSQEPGTYDPEHFTEEAPRSTIAFOSRLAQI  
SROIERNQGALAPTYLDPPLIENSYI"

Query	Match	Score	Length
Best Local Matches	Similarity	DB	9;
	11;	Mismatches	0;
	Conservative	Indels	Gaps
Qy	177	TOCCCTGGGCCCTAGAGGCTTCCACAGGTGATGCTGGGCTCTGCTGAGCTACCTAC	236
Db	1600	TCCATCGGGAGGCAAGGCCCTATCTACCTCATGAGCACGGCCCTGCCACATTCACCTAC	1659
Qy	237	AAAAGCCTCTGATTCCTAACGACTTGTGGAGCGGGGGTGACAGGACCTGCTGGTAT	296
Db	1660	ACCAATTTCTGCCTTCGGGACAGCCCTGGGCGCCGGCGCTCTGGCATCCCCAACTAC	1719
Qy	297	TATTCCTGGATGACAGCCTCGGGGTTGGAGGACATGGAGGAGGACAGCTAGAGAT	356
Db	1720	CACTTACCGAGACGACGGCTGAGATCTGGCGGCCATTGAGCTTGTCTCAGAAATC	1779
Qy	357	CATCACTTATTAACCAAGAC	380
Db	1780	GTTGGCTACTATPATCCCACTGAC	1803

Search completed: May 25, 2002, 01:27:44  
Job time: 22325 sec

Job time: 22325 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: May 24, 2002, 18:05:53 ; Search time 1935.21 Seconds  
(without alignments)  
2650.277 Million cell updates/sec

Title: W36511  
Perfect score: 380  
Sequence: 1 GCAGGCAGGAGCTCCC.....ACTTATTTACCAATGAC 380  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:/\*  
2: em\_esthun:/\*  
3: em\_estin:/\*  
4: em\_estmu:/\*  
5: em\_estov:/\*  
6: em\_estro:/\*  
7: em\_htc:/\*  
8: em\_htc:/\*  
9: gb\_est1:/\*  
10: gb\_est2:/\*  
11: gb\_htc:/\*  
12: gb\_gss:/\*  
13: em\_gss\_hum:/\*  
14: em\_gss\_inv:/\*  
15: em\_gss\_pln:/\*  
16: em\_gss\_vrt:/\*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	380	100	0	W36511
2	185.2	48.7	462	9 AAT60573
3	174.8	46.0	361	10 W10508
4	151.4	39.8	553	10 BG456248
5	131.6	34.6	645	10 BG456629
6	121.6	32.0	425	10 BG946103
7	115.0	30.3	99	9 AW488090
8	114.6	30.2	818	10 BG698713
9	100.4	26.4	795	10 BI667266
10	97.5	25.5	100	W18678
11	93.4	24.6	518	9 A1788059
12	89.8	23.6	214	10 W11802
13	88.2	23.2	214	9 BB87762
14	80.4	21.2	257	9 A038641
15	80.4	21.2	449	9 A1385442
16	75.9	19.7	277	9 BE715737
17	66.4	17.5	445	10 BF464406

ALIGMENTS

RESULT	1
W36511	W36511
LOCUS	mb76509.r1 Soares mouse p3NMF19.5 MUS MUSCULUS cDNA clone
DEFINITION	IMAGE:335569 5' similar to SW-LOX2_HUMAN p18054 ARACHIDONATE 12-LIPPOXYGENASE ; mRNA sequence.
ACCESSION	W36511
VERSION	W36511.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 380)
REFERENCE	1 (Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, K., Stoepto, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R. The WashU-HMM Mouse EST Project. Unpublished (1996))
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, K., Stoepto, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and Waterston, R. The WashU-HMM Mouse EST Project. Unpublished (1996))
TITLE	WashU-HMM Mouse EST Project
JOURNAL	WashU-HMM Mouse EST Project
COMMENT	WashU-HMM Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
FEATURES	1. .380 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:335369" /clone_110="Soares mouse p3NMF19.5"

/dev\_stage="19.5 dpc total fetus"  
/1ab host=DH10B (ampicillin resistant)"  
/notee="vector: pT73D (Pharmacia) with a modified  
polylinker; site\_1: Not I; site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dt) primer (15')  
TCTTACCAATCGAAGTGGGCGCAATTGGGTTTTTTT 3',  
double stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a COT = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA was kindly provided by  
Dr. Minoru Ko (Wayne State University)."

BASE COUNT  
ORIGIN  
79 a 102 c 106 g 93 t

Washinton University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LILN; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MG:1:654157  
Possible reversed clone: similarity on wrong strand  
Seq. Primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 357.

FEATURES  
Source

1. .462

Location/Qualifiers

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1. .462

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TITLE JOURNAL COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)	
	Unpublished (1999)	
CONTACT	Contact: Robert Strausberg, Ph.D.	
EMAIL	Email: cggps-f@mail.nih.gov	
TISSUE PROCUREMENT	CDNA Library Preparation: Ling Hong/Rubin Laboratory	
CDNA LIBRARY ARRANGED BY	DNA sequencing by: Incyte Genomics, Inc.	
DNA SEQUENCING BY	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNLL at:	
http://image.llnl.gov	http://image.llnl.gov	
PLATE	Plate: LNCM383 row: b column: 07	
HIGH QUALITY SEQUENCE STOP	High quality sequence stop: 643.	
LOCATION/QUALIFIERS	1. .645	
FEATURES SOURCE	<p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone.Lib="NIH_MGC_18"</p> <p>/tissue.type="large cell carcinoma"</p> <p>/lab_host="DHB" (phage-cell-resistant)"</p> <p>/note="Organ: lung; Vector: pORB7; Site_1: xhol; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adapter: GCGACGAG (G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."</p>	
BASE COUNT	122	a 201 c 190 g 132 t
ORIGIN	High quality sequence start: 425.	
QUERY MATCH	34.6%	Score 131.6; DB 10; Length 645;
BEST LOCAL SIMILARITY	80.6%	Pred. No. 5.7e-28;
MATCHES	166;	Mismatches 0; Indels 1; Gaps 1;
CONSERVATIVE		
QY	175	TTTCCCTGGCCCTAGAGGCTTCGCCACAGGATGGTCGGGCTCTGAGCTACCT 234
Db	425	TGTCCTCTGGCGCTGGAGCTTGCTGGGTTATGGTACGGCTCTGCGGAGTCACCT 484
QY	235	ACAAAGGCTCTCATGCCAACGACTTGTGAGCCGGGTTCCAGGACCTGGCTGGGT 294
Db	485	ATGACAGCCTCTACCTCCCCTATGACTTGTGGAGCTGGGCTGGGTTACGGCTTGAT 544
QY	295	ATATTTCGGTAGACAGCTGGCTGGAGATGGAGTACGGTACAG 354
Db	545	ATTCATACCGCGAGACACTTGCGGTTGGAGATGACTGGAGAATATGGAC-GGAG 603
355	ATCATCACTATTACCAATGAC	380
604	ATCATCACTATTACCGAGTGAC	629
BASE COUNT	77	a 99 c 155 g 94 t
ORIGIN	High quality sequence start: 425.	
QUERY MATCH	32.0%	Score 121.6; DB 10; Length 425;
BEST LOCAL SIMILARITY	82.7%	Pred. No. 4.1e-25;
MATCHES	139;	Mismatches 0; Indels 0; Gaps 0;
CONSERVATIVE		
QY	175	TTTCCCTGGCCCTAGAGGCTTCGACAGCTGGTGTGGGGCTGCTGAGCTCACCT 234
Db	175	TGTCCTCTGGGGTGGAGGGTTGCTGGAGCTGGGCTGGGTTACGGCTCTGCGGAGCTCACCT 234
QY	235	ACAAAGCCTCTGCAATCCCACGACTTGTGGAGCGCCGGGTCAGGACCTGGCTGGT 294
Db	235	ATGACAGCCTCTACCTCCCCTATGACTTGTGGAGCTGGGTCAGGACCTGGCTGGAT 294
QY	295	ATATTTCGGTAGACAGCTGGGTTGGAGATGGAGTACGGTACAG 342
Db	295	ATTCATACCGCGAGACACTTGCGGTTGGAGATGACTGGAGAAGT 342
RESULT	6	AW488090/c
LOCUS	BG946103	425 bp mRNA linear EST 11-JUN-2001
DEFINITION	MS3-KT0050-080101-001-c03	KT0050 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BG946103	
VERSION	BG946103.1	GI:1434514
KEYWORDS	EST.	
SOURCES	human.	
ORGANISM	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 425)	
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmam, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed	
JOURNAL	EST	
MEDLINE	EST	
COMMENT	National Institute of Mental Health	
sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
MEDLINE	2020663	
COMMENT	Contact: Simpson A.J.G.	
REFERENCE	Laboratory of Cancer Genetics	
AUTHORS	Ludwig Institute for Cancer Research	
TITLE	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil	
JOURNAL	Tel: +55-11-270922	
MEDLINE	Fax: +55-11-2707001	
COMMENT	Email: asimpon@ludwig.org.br	
REFERENCE	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL	
AUTHORS	(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR3&t2=MR3-KT0050-080101-001-c03&t3=2001-01-08&t4=1)	
TITLE	Seq primer: puc 18 forward	
JOURNAL	High quality sequence start: 16	
MEDLINE	High quality sequence stop: 425.	
COMMENT	Location/Qualifiers	
FEATURES SOURCE	<p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:665"</p> <p>/clone.Lib="K10050"</p> <p>/note="Organ: bladder tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-clone was made by cloning products derived from ORESSES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."</p>	
BASE COUNT	77	a 99 c 155 g 94 t
ORIGIN	High quality sequence start: 16.	
QUERY MATCH	32.0%	Score 121.6; DB 10; Length 425;
BEST LOCAL SIMILARITY	82.7%	Pred. No. 4.1e-25;
MATCHES	139;	Mismatches 0; Indels 0; Gaps 0;
CONSERVATIVE		
QY	175	TTTCCCTGGCCCTAGAGGCTTCGACAGCTGGTGTGGGGCTGCTGAGCTCACCT 234
Db	175	TGTCCTCTGGGGTGGAGGGTTGCTGGAGCTGGGTTACGGCTCTGCGGAGCTCACCT 234
QY	235	ACAAAGCCTCTGCAATCCCACGACTTGTGGAGCGCCGGGTCAGGACCTGGCTGGT 294
Db	235	ATGACAGCCTCTACCTCCCCTATGACTTGTGGAGCTGGGTCAGGACCTGGCTGGAT 294
QY	295	ATATTTCGGTAGACAGCTGGGTTGGAGATGGAGTACGGTACAG 342
Db	295	ATTCATACCGCGAGACACTTGCGGTTGGAGATGACTGGAGAAGT 342
RESULT	7	AW488090/c
LOCUS	AW488090	439 bp mRNA linear EST 24-FEB-2000
DEFINITION	UI-M-BH3-arr-e-11-0-UI-s1_NH_BMAP_M_S4	mus musculus cDNA clone
ACCESSION	UI-M-BH3-arr-e-11-0-UI	3', mRNA sequence.
VERSION	AW488090	
KEYWORDS	EST.	
SOURCE	EST.	
ORGANISM	Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
REFERENCE	1 (bases 1 to 499)	
AUTHORS	Bonaldo M.F., Lennon, G., and Soares, M.B.	
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery	
JOURNAL	Genome Res. 6 (9), 791-806 (1996)	
MEDLINE	9704477	
COMMENT	Contact: Chin, H	
REFERENCE	6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD	
AUTHORS		
TITLE		

Fax: 301 443 1705  
Tel: 301 443 9890  
Email: mest@mail.nih.gov  
Oligo-dT track not found. Not I site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
clones from RESEARCH GENETICS. It should be noted that Bento Soares  
is generating a small number of additional specialized  
non-redundant arrays of BMAP cDNAs whose availability will be  
considered under appropriate and limited collaborative arrangements  
Seq primer: M13 Forward  
POLY=A No. location/origin/strain

source  
1. 499  
/organism="Mus musculus"  
/strain="C57BL/6J"

BG698713  
 LOCUS BG698713 818 bp mRNA linear EST 07-MAY-2001  
 DEFINITION 6027030881 NCL\_CGAP\_Sku3 Homo sapiens cDNA clone IMAGE:4800620 5',  
 mRNA sequence.  
 ACCESSION BG698713  
 VERSION BG698713.1 GI:13966275  
 KEYWORDS EST.  
 SOURCE EST.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 818)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [croaps-r@mail.nih.gov](mailto:croaps-r@mail.nih.gov)  
 Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Invitri Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the T.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM10691 row: 0 column: 21  
High quality sequence stop: 779.

source  
education/qualifications  
1. .818

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>clone_1.fnb="NCI_CGGAP_Skn3"
>lab.host="DH10B (T1 phage-resistant)"
>note="Organ: Skin; Vector: pCMV-SPOR6; Site.1: NotI;
Site.2: SALL; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGGAP Library."

```

CDNA inserts from NIH\_BMAP\_M\_S3\_3, NIH\_BMAP\_M\_S3\_2, and NIH\_BMAP\_M\_S3\_1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH\_BMAP\_M\_S3\_3, NIH\_BMAP\_M\_S3\_2, and NIH\_BMAP\_M\_S3\_1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH\_BMAP\_M\_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996) TAG\_LIB-NIH\_BMAP\_M\_S4  
 TAG\_TISSUE-basal-ganglia  
 TAG\_SEQ-TGTCAC"  
 ORIGIN  
 BASE COUNT  
 107 a 139 c 142 g 111 t

Query	Match	Score	Length
Qy	TTTCCCTGGCCTAGAGGCTTCCACAGGTGAGGTCGGGCTGCTGAGCTACCT	30 2%	314 6;
Best Local Similarity	75 6%	DB 10:	818;
Matches	155;	Pred. No.	6.3e-23;
Conservative	0;	Mismatches	49;
		Indels	1;
		Gaps	1;
Db	TTTCCCTGGCCTGGAAGGCTTGTGGGTGTGAGGTCCTGCTGAGCTACCT	234	
417	TGTCCTCTGGCGCTGGAAGGCTTGTGGGTGTGAGGTCCTGCTGAGCTACCT	476	
Qy	ACAAAAGCCCTCTGATTCCTCCAACTG-ACMTTGTGAGGCGCGGTCAGGACTGCCC	293	
235	ACAAAAGCCCTCTGATTCCTCCAACTG-ACMTTGTGAGGCGCGGTCAGGACTGCCC	293	
Db	ATGACAGCCCTACCTCCCCAACTGCACTTGTGAGGCGTGGGTCCAGGACCTGCGTGA	536	
477	ATGACAGCCCTACCTCCCCAACTGCACTTGTGAGGCGTGGGTCCAGGACCTGCGTGA	536	

Query	Match	Score	Length
QY	242 CCTCTGATTCACAGGACTTGTGAGCGCGGGTCAGGACCTGCGATTATT	30.3%	499
Db	499 CCCTCTGATTCACAGGACTTGTGAGCGCGGGTCAGGACCTGCGATTATT	95.6%	301
QY	302 CGGTGATGACASCTGGGGTGTGAGCGATGGAGGATAGTGTGACTAGATCATCA	0	440
Db	439 CGGTGATGACACCTGGGGTGTGAGCGATGGAGGATAGTGTGACTAGATCATCA	129; Conservative	361
QY	362 CTTATTAATACCCAA	376	381
Db	380 CTATATTAATACCCAA	366	1;

RESULT 8

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:

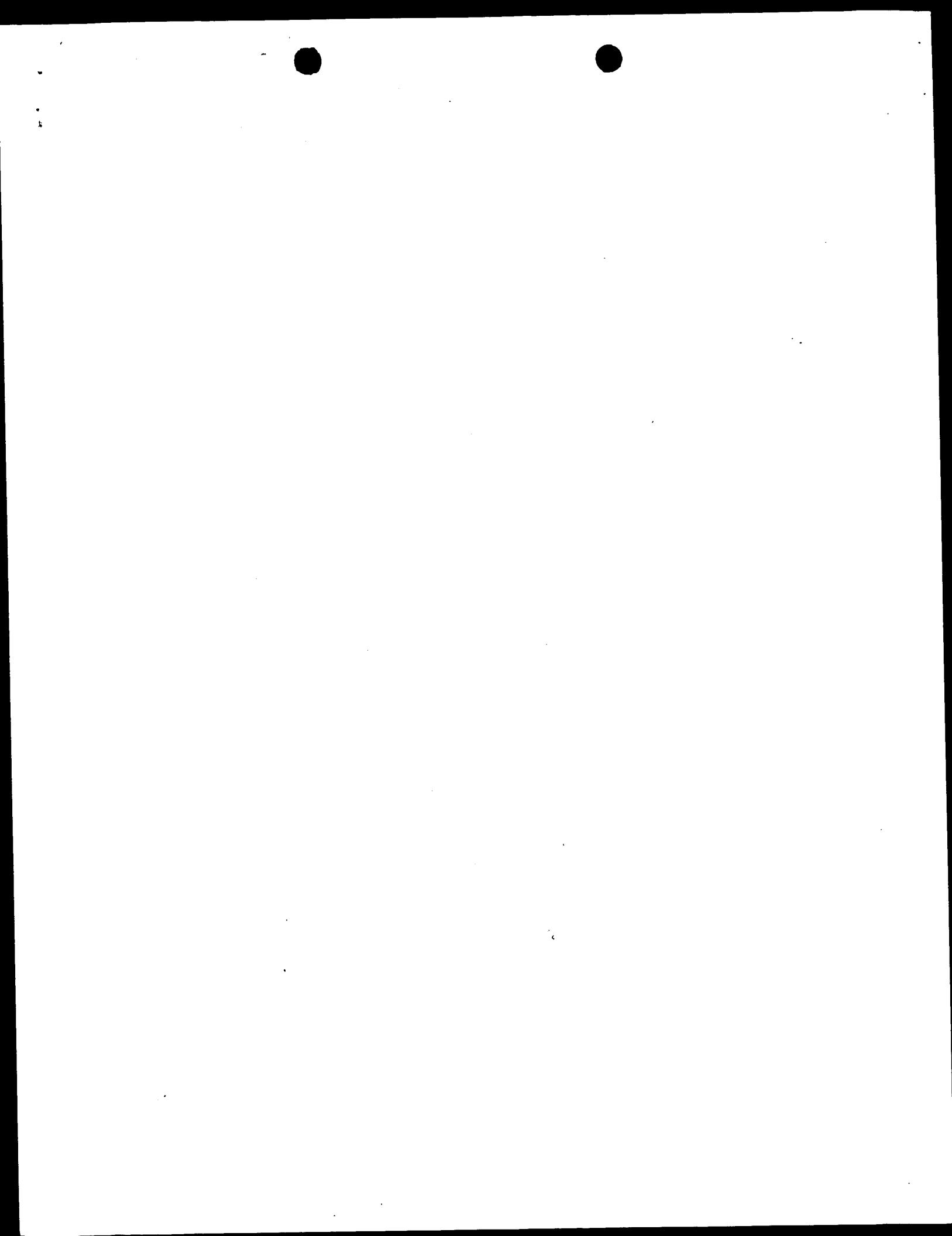
REFERENCE	TITLE	
1 (bases 1 to 795)	The WashU-HMMI Mouse EST Project.	
NIH-MCC http://mcc.nci.nih.gov/	Unpublished (1996)	
National Institutes of Health, Mammalian Gene Collection (MGC)	On Sep 12, 1996 this sequence version replaced 91:1294386.	
Unpublished (1999)	Contact: Marra M/Mouse EST Project	
COMMENT	WashU-HMMI Mouse EST Project	
Contact: Robert Strausberg, Ph.D.	Washington University School of Medicine	
Email: cagabs@mail.nih.gov	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
Tissue Procurement: Miklos Falkovits, M.D., Ph.D.	Tel: 314 286 1800	
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki	Fax: 314 286 1810	
Toshiyuki and Piero Carninci (RIKEN)	Email: mouseest@watsont.wustl.edu	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	This clone is available royalty-free through LLNL; contact the	
DNA Sequencing by: Incyte Genomics, Inc.	IMAGE Consortium (info@image.llnl.gov) for further information.	
Clone distribution: MGC clone distribution information can be	MGI:218865	
found through the I.M.A.G.E. Consortium/LLNL at:	Trace considered overall poor quality	
http://image.llnl.gov	possible reversed clone; similarity on wrong strand	
Plate: LIAM11790 row: 9 column: 06	Seq primer: -28M13 rev2 from Amersham	
High quality sequence stop: 740.	High quality sequence stop: 1.	
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SOURCE	1. . 795	
organism="Homo sapiens"		
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/tissue_type="hypothalamus"		
/lab_host="DH10B"		
/note="Organ: brain; Vector: pBluescriptR (modified		
pBluescript KS); Site_1: BamHI; Site_2: SalI-XbaI (gtcgcag		
; Oligo-primed using primer 5'-TTTTTTTTTTTTTNN-3',		
size-selected for average insert size 2.3 kb and		
normalized to ROT 5. This is a primary library enriched		
for full-length clones and constructed using the		
Cap-trapper method (Carninci, in preparation). Library		
constructed by M. Brownstein (NIMH/NHGRI, National		
Institutes of Health). Note: this is a NIH_MGC Library."		
BASE COUNT	153 a 256 c 228 g 158 t	
ORIGIN		
Query Match 26.4%	Score 100.4; DB 10; Length 795;	
Best Local Similarity 82.5%	Pred. No. 9.3e-19;	
Matches 127; Conservative 0; Mismatches 26; Indels 1; Gaps 1;		
QY 175 TTTCCCTGGCTTAGGGCTTGGCAGGGATGATCTGGCTGCTGAGGCTACCT 234		
Db 597 TGTCCCTGGCTGGAGCTTGTGGTGTAGTGTACGGCTCTGTCGAGCTACCT 656		
QY 235 ACAAAAGCTCTCATGCCAACGACTTGGAGGGCTGGTCAAGGACCTGGT 294		
Db 657 ATGACAGCTCTAC-TCCCCATGACTGAGTTGGAGCTGGGTCCAGGACCTGGAT 715		
QY 295 ATTTATTCGGTAGACAGCTGGGGTGTGGAGCTGGGTCCAGGAC 328		
Db 716 TTTACTACCGCGATGACAGCTGGGGGGTGGGA 749		
RESULT 10		
W18678 W18678 100 bp mRNA linear EST 12-SEP-1996		
LOCUS W18678		
DEFINITION p3NMF19.5 MUS musculus cDNA clone		
IMAGE:33745 5' similar to SW-LOX5_RAT P12527 ARACHIDONATE		
5-LIPOXYGENASE ; mRNA sequence.		
ACCESSION W18678		
VERSION W18678.1		
KEYWORDS EST.		
ORGANISM house mouse.		
Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE 1 (bases 1 to 100)		
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubroque,T.,		
Geissel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,		
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,		
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
Waterston,R. and Wilson,R.		
RESULT 11		
AI788059 AI788059 518 bp mRNA linear EST 02-JUL-1999		
LOCUS AI788059		
DEFINITION u116908 Y1 Sugano mouse embryo mewa Mus musculus cDNA clone		
IMAGE:2087745 5' similar to TR-070582_070582_ARACHIDONATE		
12-LIPOXYGENASE, PSEUDogene 2 ; mRNA sequence.		
ACCESSION AI788059		
VERSION AI788059.1		
KEYWORDS EST.		
ORGANISM house mouse.		
Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE 1 (bases 1 to 518)		
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,		
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person		
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter		
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,		
Waterston,R. and Wilson,R.		





Search completed: May 25, 2002, 00:50:47  
Job time: 24294 sec

Job time: 24294 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on:

May 24, 2002, 18:53:03 ; Search time 62.9 Seconds

(without alignments)  
1483.954 Million cell updates/sec

Perfect score:

1 GCAGGGCAGCTGTGCTCC...ACTTATATTACCAAAATGAC 380

Sequence:

IDENTITY.NUC  
Gapop 10.0 , Gapext 1.0

Scoring table:

383533 seqs, 122816752 residues

Searched:

1 All number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued\_Patents\_NA.\*

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6: /cgn2\_6/patdata/1/ina/backfiles1.seq,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135.8	35.7	2469	3 US-09-087-727-1	Sequence 1, Appli
2	50	13.2	2685	4 US-09-061-768A-1	Sequence 1, Appli
3	50	13.2	3205	4 US-09-061-768A-3	Sequence 1, Appli
4	33.4	8.8	2124	4 US-09-198-122-1	Sequence 1, Appli
5	33.2	8.7	20235	1 US-07-642-734C-3	Sequence 3, Appli
6	33.2	8.7	20235	1 US-08-439-09A-3	Sequence 3, Appli
7	32.4	8.5	2049	4 US-09-099-749-10	Sequence 10, Appli
8	30.8	8.1	3271	2 US-08-852-806-1	Sequence 1, Appli
9	30.8	8.1	3271	3 US-09-163-669-1	Sequence 1, Appli
10	30	7.9	3710	4 US-07-741-453A-62	Sequence 1, Appli
11	29.8	7.8	2297	1 US-08-484-493-1	Sequence 1, Appli
12	29.8	7.8	2297	1 US-08-484-494-1	Sequence 1, Appli
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14	29.8	7.8	2297	3 US-09-249-003-1	Sequence 1, Appli
15	29.8	7.8	3357	3 US-08-726-214-7	Sequence 1, Appli
16	29.4	7.7	1598	1 US-08-211-682-24	Sequence 1, Appli
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23	28.4	7.5	2968	4 US-03-813-819-1	Sequence 1, Appli
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27	28	7.4	28958	1 US-08-258-261B-6	Sequence 1, Appli

### ALIGNMENTS

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US-09-087-727-1	Sequence 1, Application US/09087727A ; Patient No. 6103496
;	GENERAL INFORMATION:
;	APPLICANT: Boeglin, William E
;	APPLICANT: Kim, Richard B
;	TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and Fatty Acid
;	FILE REFERENCE: Attorney Docket No. 6103496 1242-7
;	CURRENT APPLICATION NUMBER: US/09/087,727A
;	CURRENT FILING DATE: 1998-05-29
;	NUMBER OF SEQ ID NOS: 12
;	SOFTWARE: PatentIn Ver. 2.0
;	SEQ ID NO: 1
;	LENGTH: 2469
;	TYPE: DNA
;	ORGANISM: Homo sapiens
;	FEATURE: CDS
;	NAME/KEY: CDS
;	LOCATION: (260)..(2362)
;	US-09-087-727-1
;	Query Match
;	Score 135.8; DB 3; Length 2469;
;	Best local Similarity 83.4%; Pred. No. 4 2e-36;
;	Matches 166; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
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## GENERAL INFORMATION:

APPLICANT: BRASH, ALAN R.

APPLICANT: BOEGLIN, WILLIAM E.

APPLICANT: JISAKA, MITSUO

TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARLES A. TAYLOR, JR.

STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

CITY: DURHAM

STATE: NORTH CAROLINA

COUNTRY: USA

ZIP: 27707

COMPUTER READABLE FORM:

COMPUTER TYPE: Diskette, 3.50 inch, 1.4 MB storage

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/061,768A

FILING DATE: APRIL 16, 1998

CLASSIFICATION: 435

PRIORITY APPLICATION DATA: NONE

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 493-8000

TELEFAX: (919) 419-0383

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2685 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

US-09-061-768A-1

Query Match

Best Local Similarity

Score 50; DB 4; Length 2685;

Matches 112; Conservative

Score 56.6%; Pred. No. 4.4e-07;

Matches 0; Mismatches

Score 85; Indels 1; Gaps 1;

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Db 1367 CATGGCAGTGAAGCTTCTCTAGTATACAGGAGAACATGAGCAGTGACTATC 1426

Db 239 AAGCTCTGATCCAAAGCACTTGTGGAGCCGGGTCAGGACCTGGCTGGGTTA 298

Db 1427 TCTCTGTCCTGCTGGAGATTCGACCCGGAGGTGAGACATCCCAGGCTACTA 1486

- Qy 299 TTTCGGTACACCTGGCGTGTGGPAGGCATGAGGAGGTACGTGACAGATCA 358

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Db 1487 CTACCGTGTAGATGGATGAGCTTGGGTGCACTGGAACTTCTCTGAATCA 1545

RESULT 4  
US-09-198-122-1  
; Sequence 1, Application US/09198122  
; Patent No. 6180380

GENERAL INFORMATION:

APPLICANT: Strebhardt, Klaus; Rubsamen-Walgramm, Helga;  
GENERAL INFORMATION:  
APPLICANT: Strebhardt, Klaus; Rubsamen-Walgramm, Helga;  
APPLICANT: Boegl, Klaus; Rubsamen-Walgramm, Helga;; Sequence 3, Application US/09061768A  
; Patent No. 6204037GENERAL INFORMATION:  
APPLICANT: BRASH, ALAN R.  
APPLICANT: BOEGLIN, WILLIAM E.  
APPLICANT: JISAKA, MITSUO  
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36



NAME/KEY: misc-feature  
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 OTHER INFORMATION: /function= "approximate span of  
 OTHER INFORMATION: acyltransferase domain of module 4"  
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 LOCATION: 15172..16569  
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RESULT 6  
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 Sequence 3, Application US/08439009A  
 ; Patent No. 604787  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donadio, S  
 ; APPLICANT: Katz, L  
 ; APPLICANT: McElpine, J B  
 ; TITLE OF INVENTION: Method of Directing Biosynthesis of  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Steven F. Weinstock  
 ; STREET: Abbott Laboratories D377/AP6D-2 One Abbott  
 ; STREET: Park Rd  
 ; CITY: Abbott Park  
 ; STATE: IL  
 ; COUNTRY: US  
 ; ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/439,009A  
 FILING DATE: 11-MAY-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Casuto, Dianne  
 REGISTRATION NUMBER: 40,943  
 REFERENCE/DOCKET NUMBER: 4952.US.D1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-938-3137  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20225 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: unknown  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Saccharopolyspora erythraea

STRAIN: NRR1 238  
 FEATURE: ;  
 NAME/KEY: CDS  
 LOCATION: 19..10722  
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 OTHER INFORMATION: /function= "gene eryA"  
 OTHER INFORMATION: /product= "orf2 encoding modules 3 & 4 for  
 FEATURE: misc\_feature  
 LOCATION: 19..470  
 OTHER INFORMATION: /function= "approximate span of  
 OTHER INFORMATION: module 3"  
 FEATURE: ;  
 NAME/KEY: misc\_feature  
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 OTHER INFORMATION: /function= "approximate span of  
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 LOCATION: 10723..20235  
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 OTHER INFORMATION: /function= "gene eryA"  
 OTHER INFORMATION: /product= "orf3 encoding modules 5 & 6  
 OTHER INFORMATION: 6-deoxyerythronolide B formation"  
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 NAME/KEY: misc\_feature  
 LOCATION: 10723..15165

FEATURE: ;  
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 LOCATION: 14062..14610  
 OTHER INFORMATION: /function= "approximate span of  
 OTHER INFORMATION: beta-ketoreductase of module 5"  
 FEATURE: ;  
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 FEATURE: ;  
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 LOCATION: 15166..20235  
 OTHER INFORMATION: /function= "approximate span of  
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 OTHER INFORMATION: acyl carrier domain of module 6"  
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 OTHER INFORMATION: /function= "approximate span of  
 OTHER INFORMATION: thioesterase domain of module 6"  
 US-08-439-009A-3

Query Match 8.7%; Score 33.2; DB 3; Length 20235;  
 Best Local Similarity 52.1%; Pred. No. 0.59; Gaps 0;  
 Matches 74; Conservative 0; Mismatches 68; Indels 0;

Qy 189 GAGGGGTCCACAGGTATGGTTCGGGGCTCTCTGAGCTCACCTACAAAGCCCTCTGC 248

Db 17682 GAGCTCGGCGATCAGGTCTCCCGCGGTGCGGGGACGCCAGTCGGCAGCG 17623

Qy 249 ATTCGCAACGACTTGTGAGCGGGGGTCAGAACGCGCTGGGGATATTTCGTGAT 308

Db 17622 GTCCCGGGATCTCTGCACCCCGCGCTGAGCACGGGTGGGGTCATCTCGACGAA 17663

Qy 309 GACAGCTGGCGGTGGTACG 330

Db 17562 GTGGCGTGGACCGTCGGCAGC 17541

US-09-099-749-10  
 ; Sequence 10, Application US/09099749B  
 ; Patent No. 6306591  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Utah State University  
 ; TITLE OF INVENTION: Screening For The Molecular Defect Causing Spider Lamb  
 ; FILE REFERENCE: 3700US  
 ; CURRENT APPLICATION NUMBER: US/09/099, 749B  
 ; CURRENT FILING DATE: 1998-06-18  
 ; EARLIER APPLICATION NUMBER: 60/050, 127  
 ; EARLIER FILING DATE: 1991-06-18  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Corel Wordperfect 8.0  
 ; SEQ ID NO: 10  
 ; LENGTH: 2049  
 ; TYPE: DNA  
 ; ORGANISM: Sheep  
 ; US-09-099-749-10

RESULT 8  
 Query Match 8.5%; Score 32.4; DB 4; Length 2049;  
 Best Local Similarity 55.3%; Pred. No. 0.34; Indels 51; Gaps 0;  
 Matches 63; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
 ; Sequence 1, Application US/08852806  
 ; Patent No. 5874245  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Shoji Fukusumi  
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Shuji Hinuma  
 ; STREET: 709 Smedeland Road  
 ; CITY: King of Prussia  
 ; STATE: PA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19406-0939  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/852, 806  
 ; FILING DATE: 16 MAY 1996  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/017, 915  
 ; FILING DATE: 16 MAY 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Han, William T  
 ; REGISTRATION NUMBER: 34-344  
 ; REFERENCE/DOCKET NUMBER: TAK50002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-270-5219  
 ; TELEFAX: 610-270-5090  
 ; TELX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3271 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE:  
 ; ORIGINAL SOURCE:  
 ; US-08-852-806-1

RESULT 9  
 Query Match 8.1%; Score 30.8; DB 2; Length 3271;  
 Best Local Similarity 66.7%; Pred. No. 1.5; Indels 22; Gaps 0;  
 Matches 44; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 ; Sequence 1, Application US/09163669  
 ; Patent No. 6111076  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FUKUSUMI, SHOJI  
 ; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR (HIBC07)  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Ratner & Prestia  
 ; STREET: P.O. Box 980  
 ; CITY: Valley Forge  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19482  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ FOR Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/163, 669  
 ; FILING DATE: 30-SEP-1998  
 ; CLASSIFICATION:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/852, 806  
 ; FILING DATE: 07-MAY-1997  
 ; APPLICATION NUMBER: 60/017, 915  
 ; FILING DATE: 16-MAY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Prestia, Paul F  
 ; REGISTRATION NUMBER: 23-031  
 ; REFERENCE/DOCKET NUMBER: TAK-50002-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 610-407-0700  
 ; TELEFAX: 610-407-0700  
 ; TELX: 846169  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3271 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-163-669-1

Query Match 8.1%; Score 30.8; DB 3; length 3271;  
 Best Local Similarity 66.7%; Pred. No. 1.5; Mismatches 0; Indels 22; Gaps 0; Matches 78;保守性

QY 4 AGGCAGCAGCTGGTCCCCGCTCGAGAGGCAATCGCGGAGACTGGTTCCCGCTRACTGCT 63  
 Db 239 AGACAGCGGCGGTGGCAGACCCCTGAGGCACTGGGGCACTGTGTTAGATATCTCG 180

QY 64 CCATCA 69  
 Db 179 CCAGCA 174

RESULT 10  
 - US-07-741-453A-62  
 ; Sequence 62, Application US/07741453A  
 ; Patent No. 6228597  
 GENERAL INFORMATION:  
 APPLICANT: PARMENTIER, MARC  
 APPLICANT: LIBERT, FREDERIC  
 APPLICANT: DUMONT, JACQUES  
 APPLICANT: VASSART, GILBERT  
 TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR  
 TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS  
 NUMBER OF SEQUENCES: 62  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 STREET: 1615 L STREET, N.W.  
 CITY: WASHINGTON, D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20036

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/741,453A  
 FILING DATE: 19911015  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16773  
 REFERENCE/DOCKET NUMBER: 911913/1107/US/ST  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 62:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3710 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: cDNA  
 ; US-07-741-453A-62

Query Match 7.9%; Score 30; DB 4; Length 3710;  
 Best Local Similarity 49.4%; Pred. No. 3; Mismatches 0; Indels 0; Gaps 0; Matches 78;保守性

QY 46 TGGTCCCGCTGACTCTCCATCACTGACGCTCCATCACTCTGGCTGCTGCTGCCTTC 105  
 Db 126 TGGCTTCCCGCTGGGCTCGCCCTTGCCCTCTTGCCCTCTTGACCCCTGAGATGGTCCTCAGCT 185

QY 106 TGCTTACCAAGCTGTGCTCAGAGCTATGTCGGCAGACTGGAGAGACTAAAGACAT 165  
 Db 186 TTTCTCCACTGCTGCCCTPATGGGGAAAGGCCCTGCCGTGCTGTACTGTAGTACTT 245

QY 166 TAAAGATATTTCCGGCCTAGGGCTTCGACAG 203

Query Match 8.1%; Score 30.8; DB 1; Length 2297;  
 Best Local Similarity 51.1%; Pred. No. 2.8; Mismatches 0; Indels 67; Gaps 0; Matches 70;保守性

QY 177 TCCCTGGGCTTGTAGGGATAATGCTGAGCTTGGGGCTGGGTGCTGAGCTACCTAC 236  
 Db 272 TCCCTGGGCTTGTAGGGATAATGCTGAGCTTGGGGCTGGGTGCTGAGCTACCTAC 331

QY 237 AAAAGCTCTCCATTCACGACTTGTGGAGAGGCGGGTCAAGGACCTGCTGGTAT 296  
 Db 332 CAACGCTCTCTCTGAGATGCCCTGGCACCAACGAGTGTGCCGCCCCGAGCCGTT 391

QY 297 TATTCGGTATGAGCAG 313

RESULT 12 US-08-484,494-1  
 Sequence 1, Application US/08484494  
 Patent No. 5798339  
 GENERAL INFORMATION:  
 APPLICANT: Wilson, Peter J  
 APPLICANT: Morris, Charles P  
 APPLICANT: Anson, Donald S  
 APPLICANT: Occhiodoro, Teresa  
 APPLICANT: Blailecki, Julie  
 APPLICANT: Clements, Peter R  
 APPLICANT: Hopwood, John J  
 TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF  
 IDURONATE 2-SULFATASE  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Scully, Murphy & Presser  
 STREET: 400 Garden City Plaza  
 CITY: Garden City  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 11530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,494  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 991,973  
 FILING DATE: 17-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: D1619110, Frank S  
 REGISTRATION NUMBER: 31,346  
 REFERENCE/DOCKET NUMBER: 84162  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 516-742-4343  
 TELEFAX: 516-742-4366  
 TELE: 230 901 SANS UR  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2297 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 125..1774  
 US-08-484-494-1

RESULT 13 US-08-345-212-1  
 Sequence 1, Application US/08345212  
 Patent No. 5932211  
 GENERAL INFORMATION:  
 APPLICANT: Wilson, Peter J  
 APPLICANT: Morris, Charles P  
 APPLICANT: Anson, Donald S  
 APPLICANT: Occhiodoro, Teresa  
 APPLICANT: Blailecki, Julie  
 APPLICANT: Clements, Peter R  
 APPLICANT: Hopwood, John J  
 TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF  
 IDURONATE 2-SULFATASE  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Scully, Murphy & Presser  
 STREET: 400 Garden City Plaza  
 CITY: Garden City  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 11530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/345,212  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 991,973  
 FILING DATE: 17-DEC-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: D1619110, Frank S  
 REGISTRATION NUMBER: 31,346  
 REFERENCE/DOCKET NUMBER: 84162  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 516-742-4366  
 TELEFAX: 516-742-4366  
 TELE: 230 901 SANS UR  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2297 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 125..1774  
 US-08-345-212-1

Query Match 7.8%; Score 29.8; DB 1; \*Length 2297;  
 Best Local Similarity 51.1%; Pred. No. 2.8;  
 Matches 70; Conservative 0; Mismatches 0;  
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 QY 272 TCCCTGGGCTTATGGGATAAGCTGGTGGAGGCTCCAAATATGCCAACCTGGATCC 331  
 QY 237 AAAAGCCTCTCATCCACAGCTTGCGACGCCGGTCCAGGACCTGGCTGGTGGAT 296  
 QY 237 AAAAGCCTCTCATCCACAGCTTGCGACGCCGGTCCAGGACCTGGCTGGTGGAT 296  
 QY 332 CACAGCTCTCATCCACAGATGCCAACGAGCTGGCTGGCAGCAASCGTGTGGCGCCCGAGCCGCGT 391  
 QY 297 TATTCGTTGATGACAG 313  
 Db 392 TCTTCTCTACTGGCAG 408

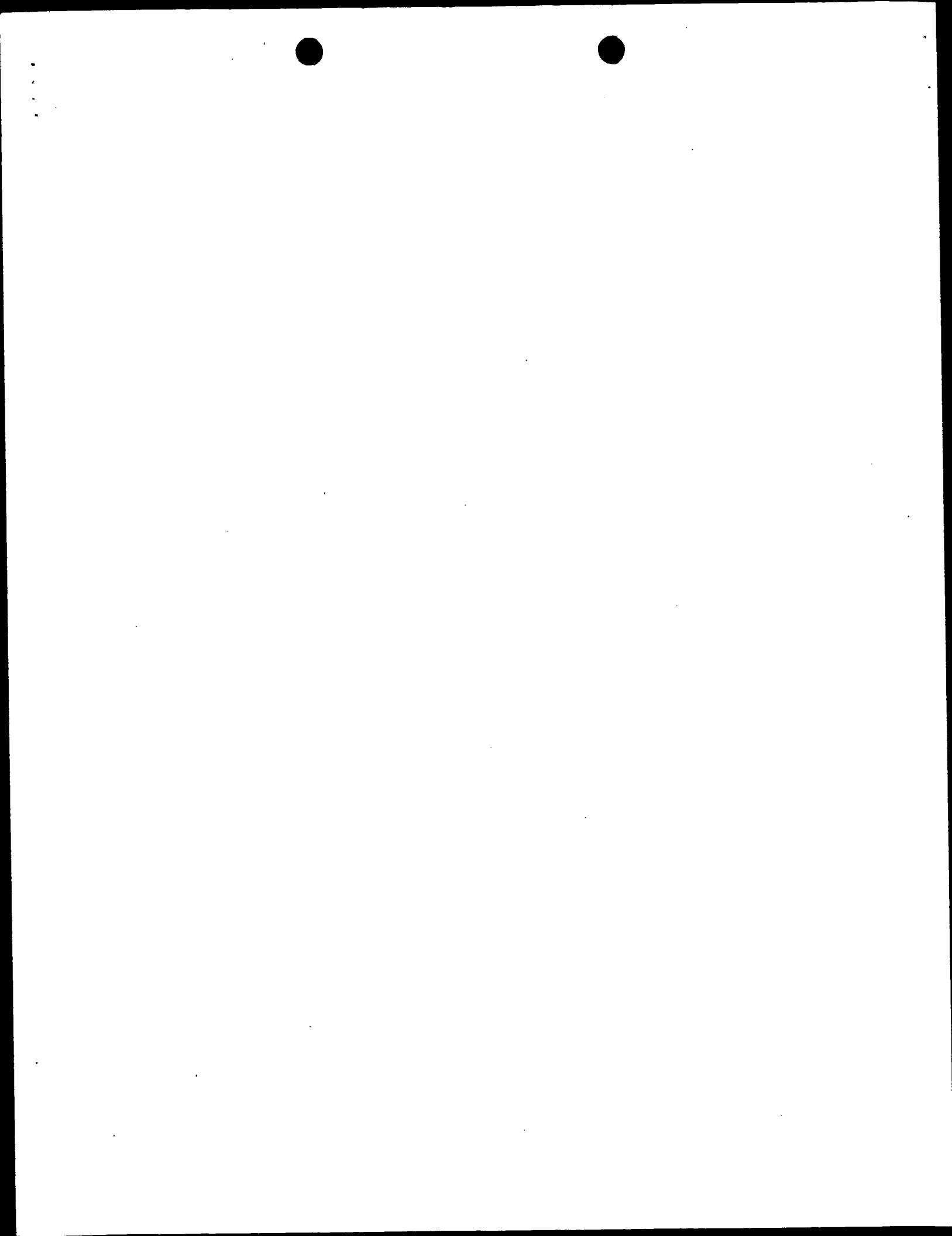
RESULT 14  
US-09-249-003-1  
Sequence 1, Application US/09249003  
; Patent No. 6153188  
GENERAL INFORMATION:  
APPLICANT: Wilson, Peter J  
Morris, Charles P  
APPLICANT: Alison, Donald S  
Occhioloro, Teresa  
APPLICANT: Blieck, Julie  
APPLICANT: Clements, Peter R  
APPLICANT: Hopwood, John J  
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF  
TITLE OF INVENTION: IDONORATE 2-SULFATASE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Preiser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: USA  
ZIP: 11530  
COMPILER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
APPLICATION NUMBER: US/09/249,003  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/991,973  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: DIGI910, Frank S  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 84162  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-742-4343  
TELEFAX: 516-742-4666  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2297 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 125..1774  
US-09-249-003-1

Query Match 7.8%; Score 29.8; DB 3; Length 2297;  
Best Local Similarity 51.1%; Pred. No. 2.8;  
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
Qy 177 TCCCTGGCCCTAGAGGGCTTCGCAAGGGTATGGCTCGAGCTTCACCTAC 236  
Db 272 TCCCTGGCCCTAGAGGGCTTCGCAAGGGTATGGCTCGAGCTTCACCTAC 331  
Qy 237 AAAAGCTCTGATTCCTCAACAGACTTGTGAGGAGCTGCTGCTGAGCTACCTAC 296  
Db 332 CACAGCTCCCTTCAGAATGCTTGTGGCAGAGGAGTGTGCTGGCCGAGCCCGTT 391  
Qy 297 TATTCGGTGTGAGACAG 313  
Db 392 TCTTCCTCACTGGCAG 408

Query Match 7.8%; Score 29.8; DB 3; Length 3357;  
Best Local Similarity 50.3%; Pred. No. 3.3; Length 3357;  
Matches 73; Conservative 0; Mismatches 72; Indels 0; Gaps 0;  
Qy 180 CTGGGCTAGAGGGCTCGCACAGCTGATGGTTCGGGCTCTGCTGAGCTACCTACAA 239  
Db 962 CTGGCCAGTGTGTTCCCTAAGGAGCTGCTAAATGCTCATGAACTCTTGCGCAA 1021  
Qy 240 AGCCCTGCAATTCCAAACGACTTGTGGACGGGGTCCAGGACCTCTGGTATTAT 299  
Db 1022 TTGGACCAAATGCAAGGAGCAATGTCATGGATCAAGTCCCTGGAGACTGTGTAC 1081  
Qy 300 TTCCGTGATGACAGCTGGGGT 324  
Db 1082 TACTGATGCCGCTGCCCT 1106

Search completed: May 25, 2002, 00:52:16  
Job time: 21553 sec

RESULT 15  
US-08-726-214-7  
Sequence 7, Application US/08726214  
; Patent No. 6107076  
GENERAL INFORMATION:  
APPLICANT: Yang, Wei-Jen  
APPLICANT: Gilman, Alfred G  
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
TITLE OF INVENTION: AND USES THEREFOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPILER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: 37,642  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 471-7577  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3357 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
05-08-726-214-7



GenCore version 4.5  
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Om nucleic - nucleic search, using sw model

Run on:

May 24, 2002, 23:55:26 ; Search time 315.63 Seconds

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Sequence:

IDENTITY.NUC  
Gapop 10.0 , Gapext 1.0

Scoring table:

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Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1989.DAT:\*

11: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1990.DAT:\*

12: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1991.DAT:\*

13: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1992.DAT:\*

14: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1993.DAT:\*

15: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1994.DAT:\*

16: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1995.DAT:\*

17: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1996.DAT:\*

18: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1997.DAT:\*

19: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1998.DAT:\*

20: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1999.DAT:\*

21: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2000.DAT:\*

22: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2001.DAT:\*

23: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2002.DAT:\*

### SUMMARIES

Result No. Score Match Length DB ID Description

1 135.8 35.7 2469 21 AAC55659 DNA encoding a human CDNA encoding a human

2 55.2 14.5 588 21 AAC61756

3 55.2 14.5 1383 21 AAC61752

4 55.2 14.5 1441 21 AAC61753

5 55.2 14.5 1848 21 AAC61751

6 55.2 14.5 2236 21 AAC61749

7 55.2 14.5 2316 21 AAC61760

8 55.2 14.5 2604 21 AAC61758

9 55.2 14.5 2701 21 AAC61747

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OS Homo sapiens.

XX

Post-processing:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq.032802:\*

1: /net/abs05/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1980.DAT:\*

2: /net/abs05/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1981.DAT:\*

3: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1982.DAT:\*

4: /net/abs05/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1983.DAT:\*

5: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1984.DAT:\*

6: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1985.DAT:\*

7: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1986.DAT:\*

8: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1987.DAT:\*

9: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1988.DAT:\*

10: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1989.DAT:\*

11: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1990.DAT:\*

12: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1991.DAT:\*

13: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1992.DAT:\*

14: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1993.DAT:\*

15: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1994.DAT:\*

16: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1995.DAT:\*

17: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1996.DAT:\*

18: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1997.DAT:\*

19: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1998.DAT:\*

20: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA1999.DAT:\*

21: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2000.DAT:\*

22: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2001.DAT:\*

23: /net/abs06/SIDS1/gcdata/hold-geneseq/geneseq-emb1/NA2002.DAT:\*

### ALIGNMENTS

Result No.

Score

Match

Length

DB

ID

Description

RESULT 1  
AA59659

ID AA59659 standard; DNA; 2469 BP.

XX AAA59659;

XX

Human lipoxygenase  
CDNA encoding a human lipoxygenase  
Human 15S lipoxygenase  
Human 15S lipoxygenase  
Mouse 8S-lipoxygenase  
Arachidonic acid  
Arachidonic acid  
Arachidonic acid  
Rice apoptosis induced  
Human lung tumour  
Human DNA sequence of S. eryra region of S. DNA encoding novel  
Human OREX ORF38  
Human chromosome 6  
Human immune/haema  
Sheep fibroblast  
Thermus thermophilic DNA sequencing  
Human shear stress  
Human cDNA clone  
Human CDNA clone  
Human immune/haema  
Human G protein co  
Human BA12 gene.  
Human gene express  
Mazile Jahi homolog  
Osteoarthritis tis  
Human CDNA clone  
Pseudomonas aeruginosa















QY	359	TCACTTATTTATTATGCCAATGAC	380
Db	1506	cagaatctactatccaaatggac	1527

RESULT 15  
AAC58018  
ID AAC58018 standard: DNA: 3343 RD

XX  
AC  
AAC58018;  
25-JAN-2001 (first entry)

## DE Arachidonic acid metabolism

Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridization; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridization assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.

WO200047771-A2.

11-FEB-2000; 2000KO-IR00184.  
12-FEB-1999; 990HS-0119917.  
23-MAR-1999; 990HS-0375267.  
07-MAY-1999; 990HS-0133200.  
(GEST ) GENSET.  
Blumenfeld M, Bouguerleret L  
WPI: 2000-571881-53.  
P-P5DB; RAB24019.

Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -  
Claim 70: Page 797-799. 803m. French

The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridization assays, sequencing assays and specific amplification assays for identifying an eicosanoid-related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAG5367 to AAG5818 and AAB4019 and AAB2420 represent sequences used in the exemplification of the present invention.

**N.B.** Polymorphic bases. (single nucleotide polymorphisms also known as SNPs) in the polynucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic base of C or T has been given as Y.

Q Sequence 2343 BP; 511 A; 688 C; 636 G; 495 T; 13 other;

Query Match	11.7%	Score 44.6;	DB 21;	Length 2343;
Best Local Similarity	51.3%	Pred. No. 0	0 00039;	
Matches	101;	Conservative	1;	Mismatches 95;
Qy	183	GGCCTAGGGCTTCGACAGGTATGGTTCGGGCTGTGTGAGCTACACTACAAAGC	242	Indices 0; Gaps 0;
Db	1300	gggtggggggcatgtacagtgtgtcccgtcggggggcaactcgactgtactgtcc	1359	
Qy	243	CTCTGCATTCCTAACGACTTGTGAGCGGGTCAGGACCCCTGGTATTTTC	302	
Db	1360	ctctgtctctctgtacgacactgtgtgacggggctgtggactcccaagggtcttat	1419	
Qy	303	CCTGATGACAGCTGGCGTGGTACGCCATGGAGAGGTAGTGTACTAGAGATCATC	362	
Db	1420	gcctcatgtatgtttacggcttggggatcatgtgcaggatgtggggatgtgcac	1479	
Qy	363	TATTTATCCAAATGA	379	
Db	1480	ctctttacccaragga	1496	

Query Match	11.7%	Score 44.6;	DB 21;	Length 2343;
Best Local Similarity	51.3%	Pred. No. 0	0.00039;	
Matches	101;	Conservative	1;	Mismatches
QY	183	GGCCTAGGGGCTTGCACAGTGCTGGGSGTCGTTGAGCTACATAAACG	242	
Db	1300	gttgaggggccatgtacagggtgtctcgccggggcgactcaactgtactgtcc	1359	
QY	243	CTCTGCATTCGCCAACGACTTGTGGAGCCGGGTCAGGACTGGCTGGTTATTATTC	302	
Db	1360	ctctgtcttcctgcacacctgtgcacccgtgcggccgtgcgtggactccacgtgtctctat	1419	
QY	303	CTGATGACAGCTGGGGTGTGGTACGCCATGGAGAGGTACGTGACTAGATCATCAC	362	
Db	1420	ggccatgtgttacggctctggagatattgcacaggatgtggaggatcgtccac	1479	
QY	363	TTATTATACCAATAA	379	
Db	1480	ctcttcattaccatragga	1496	

